In the Claims

Applicant has revised the claims showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts and/or double bracketing.

Please add new claims 149-164 as noted below.

1. (Previously presented) A method for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample, the method comprising:

preparing a reduced complexity genome (RCG) from the genomic sample, wherein the RCG is native RCG, and

analyzing the RCG for the presence or absence of a SNP allele.

2. (Original) The method of claim 1, wherein the analysis comprises hybridizing a SNP-ASO and the RCG, wherein the SNP-ASO is complementary to one allele of a SNP, whereby the allele of the SNP is present in the genomic sample if the SNP-ASO hybridizes with the RCG, and wherein the presence or absence of the SNP is used to characterize the genomic sample.

3. (Original) The method of claim 2, wherein the RCG is immobilized on a surface.

4. (Original) The method of claim 2, wherein the SNP-ASO is immobilized on a surface.

5. (Original) The method of claim 2, wherein the SNP-ASO is individually hybridized with a plurality of RCGs.

6-7. (Canceled)

8. (Previously presented) The method of claim 1, wherein the method further comprises identifying a genotype of the genomic sample, whereby the genotype is identified by the presence or absence of the alleles of the SNP in the RCG.

9. (Previously presented) The method of claim 1, wherein the genomic sample is obtained from a tumor.

10. (Original) The method of claim 9, wherein a plurality of RCGs are prepared from genomic samples isolated from a plurality of subjects and the plurality of RCGs are analyzed for the presence of the SNP.

11. (Original) The method of claim 8, wherein the presence or absence of the SNP allele is analyzed in a plurality of genomic samples selected randomly from a population, the method further comprising determining the allelic frequency of the SNP allele in the population by comparing the number of genomic samples in which the allele is detected and the number of genomic samples analyzed.

12.-16. (Canceled)

17. (Original) The method of claim 2, wherein at least a fraction of the SNP-ASO is labeled.

18. (Original) The method of claim 17, wherein an excess of a non-labeled SNP-ASO is added during the hybridization step, wherein the non-labeled oligonucleotide is complementary to a different allele of the same SNP than the labeled SNP-ASO.

19. (Original) The method of claim 17, further comprising performing a parallel hybridization reaction wherein the RCG is hybridized with a labeled SNP-ASO, wherein the oligonucleotide is complementary to a different allele of the same SNP than the labeled SNP-ASO.

20. (Currently amended) The method of claim 19, wherein the two SNP-~~AGOs~~ ASOs are distinguishably labeled.

21. (Original) The method of claim 17, an excess of non-labeled SNP-ASO is present during the hybridization.

22. (Original) The method of claim 2, wherein the SNP-ASO is composed of from about 10 to about 50 nucleotides residues.

23. (Original) The method of claim 22, wherein the SNP-ASO is composed of from about 10 to about 25 nucleotides residues.

24. (Original) The method of claim 17, wherein the label is a radioactive isotope.

25. (Original) The method of claim 24, further comprising the step of exposing the RCG to a film to produce a signal on the film which corresponds to the radioactively labeled hybridization products if the SNP is present in the RCG.

26. (Original) The method of claim 17, wherein the label is a fluorescent molecule.

27. (Original) The method of claim 26, further comprising the step of exposing the RCG to an automated fluorescence reader to generate an output signal which corresponds to the fluorescently labeled hybridization products if the SNP is present in the RCG.

28. (Original) The method of claim 17, wherein a plurality of SNP-ASOs are labeled with fluorescent molecules, each SNP-ASO being labeled with a spectrally distinct fluorescent molecule.

29. (Original) The method of claim 28, wherein the number of SNP-ASOs having a spectrally distinct fluorescent molecule is at least two.

30. (Original) The method of claim 28, wherein the number is selected from the group consisting of three, four and eight.

31. (Original) The method of claim 2, wherein a plurality of RCGs are labeled with fluorescent molecules, each RCG being labeled with a spectrally distinct fluorescent molecule, and wherein all of the RCGs having a spectrally distinct fluorescent molecule.

32.-34. (Canceled)

35. (Original) The method of claim 2, wherein the RCG is labeled.

36. (Original) The method of claim 4, wherein a plurality of different SNP-ASOs are attached to the surface.

37. (Canceled)

38. (Original) The method of claim 2, wherein the genomic sample is characterized by generating a genomic pattern based on the presence or absence of the allele of the SNP in the genomic sample.

39. (Original) The method of claim 38, wherein the genomic pattern is a genomic classification code.

40. (Previously presented) The method of claim 1, further comprising:
isolating genomic DNA from tumor samples obtained from a plurality of subjects,
preparing the RCGs from each genomic DNA,
performing a hybridization reaction with a SNP-ASO and the plurality of RCGs, wherein the SNP-ASO is complementary to one allele of a SNP, and
characterizing the tumor based on whether the SNP-ASO hybridizes with at least some of the RCGs, whereby if the SNP oligonucleotide hybridizes with at least some of the RCGs, then the allele of the SNP is present in the genomic DNA of the tumor.

41. (Original) The method of claim 40, wherein the hybridization reaction is performed with a plurality of SNP-ASOs immobilized on a surface, and wherein the hybridization is performed on the plurality of RCGs, each RCG being analyzed separately.

42.-46. (Canceled)

47. (Previously presented) The method of claim 1 further comprising:
preparing the RCG from an individual genome, and

generating a genomic pattern for the individual genome based on the presence or absence of SNP alleles.

48. (Original) The method of claim 47, wherein analyzing the RCG involves a hybridizing the RCG with a panel of SNP-ASOs, each of which is complementary to one allele of a SNP, and identifying the genomic pattern by determining the ability of the RCG to hybridize with each SNP-ASO.

49. (Original) The method of claim 47, wherein the genomic pattern is a genomic classification code which is generated from the pattern of SNP alleles for each RCG.

50. (Original) The method of claim 49, wherein the genomic classification code is also generated using the allelic frequency of the SNPs.

51. (Original) The method of claim 47, wherein the genomic pattern is a visual pattern.

52. (Original) The method of claim 47, wherein the genomic pattern is a digital pattern.

53. (Original) The method of claim 48, wherein the SNP-ASOs are immobilized on a surface.

54. (Original) The method of claim 47, further comprising performing a parallel reaction wherein the hybridization reaction is performed using a panel of labeled complementary SNP-ASOs.

55. (Original) The method of claim 54, wherein the RCG is immobilized on a surface and wherein each SNP-ASO of the panel is hybridized with a separate surface.

56. (Original) The method of claim 54, wherein the RCGs is immobilized on a surface and wherein a plurality of SNP-ASOs of the panel are hybridized with a single surface, each SNP-ASO being labeled with a spectrally distinct fluorescent molecule.

57.-139. (Canceled).

140. (Previously presented) The method of claim 1 further comprising:

preparing-the RCG from the genomic sample obtained from a subject , and assessing whether the subject is at risk for developing a disease based on the presence or absence of a plurality of SNP alleles that occur in at least 10% of genomes obtained from individuals afflicted with the disease occur, in the RCG.

141-147. (Canceled)

148. (Previously presented) The method of claim 1 further comprising:

preparing individual RCGs obtained from members of one or more families , determining the presence or absence of SNP alleles in the RCGs, and

comparing the RCGs of the family members by comparing the presence or absence of the SNP alleles in the RCGs of the family members.

149. (New) A method comprising:

preparing a randomly primed PCR-derived reduced complexity genome (RCG) using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,

contacting SNP-ASOs immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer and

determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a genotype.

150. (New) The method of claim 149, wherein the RCG contains less than 5% of genomic material present in a whole genome.

151. (New) The method of claim 149, wherein the RCG contains less than 1% of genomic material present in a whole genome.

152. (New) The method of claim 149, wherein the RCG contains less than 0.05% of genomic material present in a whole genome.

153. (New) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for DOP-PCR.

154. (New) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for adapter-PCR.

155. (New) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 50 nucleotide residues.

156. (New) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 25 nucleotide residues.

157. (New) A method comprising:

preparing a randomly primed PCR-derived reduced complexity genome (RCG) from a genome of a tumor cell using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,

contacting SNP-ASOs immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci associated with SNPs corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer, and

determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a loss of heterozygosity in the tumor.

158. (New) The method of claim 157, wherein the RCG contains less than 5% of genomic material present in a whole genome.

159. (New) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for DOP-PCR.

160. (New) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for adapter-PCR.

161. (New) An article in one or more containers, comprising

at least one polymerase chain reaction (PCR) primer for preparing a randomly primed PCR-derived reduced complexity genome (RCG), wherein the RCG contains less than 20% of genomic material present in a whole genome, and

a set of SNP-ASOs immobilized on a surface, wherein polymorphic loci corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer,

the article designed for use with a method of any one of claims 149 and 157.

162. (New) The article of claim 161, wherein the RCG contains less than 5% of genomic material present in a whole genome.

163. (New) The article of any one of claims 161-162, wherein the at least one PCR primer is a primer for DOP-PCR.

164. (New) The article of any one of claims 161-162, wherein the at least one PCR primer is a primer for adapter-PCR.